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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|--|-------------|----------------------|-----------------------------|------------------------|
| 10/036,729 | 12/21/2001 | Jaap M. Middeldorp | 9310-13DVCTDV | 6359 |
| 20792 7590 10/16/2007 MYERS BIGEL SIBLEY & SAJOVEC PO BOX 37428 RALEIGH, NC 27627 | | | EXAMINER LI, QIAN JANICE | |
| | | | ART UNIT 1633 | PAPER NUMBER |
| | | | MAIL DATE 10/16/2007 | DELIVERY MODE PAPER |

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

| | | | | |
|------------------------------|------------------------|--|---------------------|--|
| Office Action Summary | Application No. | | Applicant(s) | |
| | 10/036,729 | | MIDDELDORP ET AL. | |
| | Examiner | | Art Unit | |
| | Q. Janice Li, M.D. | | 1633 | |

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 23 July 2007.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 6-9, 26, 27 and 32-34 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 6-9, 26, 27 and 32-34 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____ |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

The amendment and response filed 7/23/2007 are acknowledged. Claim 34 has been amended. Claims 6-9, 26, 27, 32-34 are pending and under current examination.

Unless otherwise indicated, previous rejections that have been rendered moot in view of the amendment to pending claims or persuasive arguments will not be reiterated. The arguments in 7/23/07 response would be addressed to the extent that they apply to current rejection.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 6, 9 stand rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

In the remarks, the applicant first asserts,

In claim 6, the nucleic acid sequences encode peptides comprising an epitope of the VCA-p18 or VCA-p40 protein.

In response, it is noted claim 6 as written, the nucleic acid sequence encodes a peptide that is immunochemically reactive with antibodies to VCA-18 or VCA-p40. Hence, the genus embraced by the claimed nucleic acids may encompass coding sequences for peptides comprising an epitope of the VCA-p18 or VCA-p40, but they are not limited by such coding sequence, rather the genus encompasses nucleic acid sequences encoding any protein as long as it is immunochemically reactive with antibodies to VCA-18 or VCA-p40, which include proteins having no clear relationship to VCA proteins. Claim 6 contains multiple phrases further limiting the antibodies, but not further limiting the peptide itself. The only limitation to the peptide is its immunochemical reactivity to the antibodies. One cannot extrapolate the structures of the protein genus from the immune reactivity.

Applicants then argues that the antibodies are further defined by particular hybridoma, and one of skill in the art further recognizes that monoclonal antibodies are specific to a single epitope and all of the antibodies produced from a single hybridoma are identical.

In response, it is noted that the antibodies are not limited by the recited hybridomas, but rather limited by the immunochemical reactivity: "*are antibodies having the same reactivity with VCA-p18 as antibodies produced by the hybridoma...*".

Even assuming *arguendo* claims are directed to peptides reactive with the antibodies produced by the recited hybridoma, the peptides encompass a genus of amino acid sequences, whose nucleic acid coding sequences are limited only by the fact that they contain a nucleotide, whose expression product has certain immune

Art Unit: 1633

reactivity, while since there is no length limitation on the nucleic acid sequences, they could be a genomic sequence or a fusion protein sequence, or any other known or unknown nucleic acid sequences that happen to encode a protein reactive to the antibodies or contain sequences sharing homology with SEQ ID Nos: 1 and/or 3. Thus, even if the antibodies produced by the hybridoma have the same reactivity with VCA-18 or VCA-40, the proteins reactive to the antibodies may be structurally distinct. This could be seen in the example of the specification, where serum proteins reactive with applicant's antibody have different domain combinations, i.e structurally different (see e.g. table I of the specification).

Applicants then argue that the specification demonstrates actual reduction to practice of the nucleic acids of claim 6 as exemplified by peptides represented by various SEQ ID Nos: 2, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 and 22.

In response, it is noted that majority of the numbered peptides are only a partial sequence of a protein, which each has an amino acid sequence distinct from the other, yet they all demonstrated immune reactivity with a VCA-p18 antibody. Among the 15 proteins listed in table I, only proteins from serum No. 9 and 10 have the same combination of domains I, II, & III, yet still it's unclear whether they have the same protein sequences in the remaining portion of the immune reactive protein. One skilled in the art could not extrapolate the full-length protein sequences from the disclosure of the partial sequences and their immune reactivity. Thus, working examples of the specification, especially table I further supports the Office position, the specification fails

Art Unit: 1633

to provide an adequate description for the genus of the nucleic acid sequences encompassed by the claims.

An adequate written description for a genus of nucleic acid sequences encompassed by instant claims requires more than a mere statement that they are part of the invention, what is required is a description of the sequences themselves. The court has made it very clear "CONCEPTION OF CHEMICAL COMPOUND REQUIRES THAT INVENTOR BE ABLE TO DEFINE COMPOUND SO AS TO DISTINGUISH IT FROM OTHER MATERIALS, AND TO DESCRIBE HOW TO OBTAIN IT, RATHER THAN SIMPLY DEFINING IT SOLELY BY ITS PRINCIPAL BIOLOGICAL ACTIVITY". *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016 (Fed. Cir. 1991).

The Revised Interim Guidelines state "THE CLAIMED INVENTION AS A WHOLE MAY NOT BE ADEQUATELY DESCRIBED IF THE CLAIMS REQUIRE AN ESSENTIAL OR CRITICAL ELEMENT WHICH IS NOT ADEQUATELY DESCRIBED IN THE SPECIFICATION AND WHICH IS NOT CONVENTIONAL IN THE ART" (Column 3, page 71434), "WHEN THERE IS SUBSTANTIAL VARIATION WITHIN THE GENUS, ONE MUST DESCRIBE A SUFFICIENT VARIETY OF SPECIES TO REFLECT THE VARIATION WITHIN THE GENUS", "IN AN UNPREDICTABLE ART, ADEQUATE WRITTEN DESCRIPTION OF A GENUS WHICH EMBRACES WIDELY VARIANT SPECIES CANNOT BE ACHIEVED BY DISCLOSING ONLY ONE SPECIES WITHIN THE GENUS" (Column 2, page 71436).

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that "APPLICANT MUST CONVEY WITH REASONABLE CLARITY TO THOSE SKILLED IN THE ART THAT, AS OF THE FILING DATE SOUGHT, HE OR SHE WAS IN POSSESSION OF THE INVENTION. THE INVENTION IS, FOR PURPOSES OF THE 'WRITTEN DESCRIPTION' INQUIRY, *WHATEVER IS NOW CLAIMED*." (See page 1117.) The

specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116).

One cannot describe what one has not conceived., See *Fiddes v. Baird*, 30 USPQ2d 1481, 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

In view of these considerations, a skilled artisan would not have viewed the teachings of the specification as sufficient to show that the applicant was in possession of the claimed invention commensurate to its scope because it does not provide adequate written description for the genus sequences encompassed by the claims. Therefore, for reasons of record and set forth *supra*, the rejection stands.

Claims 6, 9 stand rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention, for reasons of record and set forth *supra*.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 6-9, 26, 27, 32-34 stand rejected under 35 U.S.C. 102(b) as being anticipated by *Laux et al.* (The EMBO J 1988;7:769-74).

Laux et al. teaches a nucleic acid sequence comprising a subsequence of instant SEQ ID No: 1 (residues 1-535 of SEQ ID No: 1), which encodes at least 12 contiguous amino acids of EBV VCA-p18 (the amino acid sequence SEQ No: 5), which would be immunochemically reactive with antibodies to the EBV VCA-p18. *Laux et al.* also teaches a nucleic acid sequence comprising instant SEQ ID No: 3, which encodes 12 contiguous amino acids of an EBV VCA-40. *Laux et al.* discloses a vector comprising the sequences (e.g. fig. 1). Accordingly, *Laux et al.* anticipates instant claims.

In the remarks, the applicant asserts that multiple alignments were performed and homology as stated in the Office action was not found.

In response, the printed copy of the database search result is hereby enclosed, which contains the details of the alignment.

Claims 6-9, 26, 27, 32-34 stand rejected under 35 U.S.C. 102(b) as being anticipated by *Bankier et al.* (Mol Biol Med 1983;1:425-445).

Bankier et al. teaches a nucleic acid sequence comprising a subsequence of instant SEQ ID No: 1 (residues 1-535 of SEQ ID No: 1), which encodes at least 12 contiguous amino acids of EBV VCA-p18 (the amino acid sequence SEQ No: 5), which would be immunochemically reactive with antibodies to the EBV VCA-p18. *Bankier et al.* also teaches a nucleic acid sequence comprising a sequence that shares 98.8%

Art Unit: 1633

homology with instant SEQ ID No: 3 (subsequence thereof), which encodes 12 contiguous amino acids of an EBV VCA-40. *Bankier et al.* discloses that the sequences were cloned in a vector (e.g. figs. 1-3). Accordingly, *Bankier et al.* anticipates instant claims.

In the remarks, the applicant asserts that multiple alignments were performed and homology as stated in the Office action was not found.

In response, the printed copy of the database search result is hereby enclosed, which contains details of the alignment.

No claim is allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

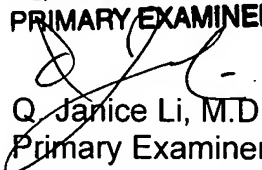
A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Q. Janice Li** whose telephone number is **571-272-0730**. The examiner can normally be reached on 9:30 am - 7 p.m., Monday through Friday, except every other Wednesday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Joseph Woitach** can be reached on **571-272-0739**. The fax numbers for the organization where this application or proceeding is assigned are **571-273-8300**.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547. For all other customer support, please call the USPTO Call Center (UCC) at **800-786-9199**.

Q. JANICE LI, M.D.
PRIMARY EXAMINER


Q. Janice Li, M.D.
Primary Examiner
Art Unit 1633

QJL
October 10, 2007

Seq 3 of 10/036,729

Qy 661 CACTCGGGGCTTACGGATTTTCAGCCTCATCAAAGCTACGAAGTGCCCGAGATACGTCCCT 720
 |||
 Db 137078 CACTCGGGGCTTACGGATTTTCAGCCTCATCAAAGCTACGAAGTGCCCGAGATACGTCCCT 137137

Qy 721 CATCCGCCCCCACCACCAACTTCTCACCAGGCAGCTCAGGCGCAGCCTCCACCCCCGGGC 780
 |||
 Db 137138 CATCCGCCCCCACCACCAACTTCTCACCAGGCAGCTCAGGCGCAGCCTCCACCCCCGGGC 137197

Qy 781 ACACAGGCCCCCGAAGCCCACTGTGTGGCCGAGTCCACGATCCCTGAGGCGGGAGCAGCC 840
 |||
 Db 137198 ACACAGGCCCCCGAAGCCCACTGTGTGGCCGAGTCCACGATCCCTGAGGCGGGAGCAGCC 137257

Qy 841 GGGAAGTCTGGACCCCGGGAGGACACCAACCCTCAGCAGCCCCACCACCGAGGGCCACCAC 900
 |||
 Db 137258 GGGAAGTCTGGACCCCGGGAGGACACCAACCCTCAGCAGCCCCACCACCGAGGGCCACCAC 137317

Qy 901 CGCGGAAAGAAACTGGTGCAGGCCTCTGCGTCCGGAGTGGCTCAGTCTAAGGAGCCCACC 960
 |||
 Db 137318 CGCGGAAAGAAACTGGTGCAGGCCTCTGCGTCCGGAGTGGCTCAGTCTAAGGAGCCCACC 137377

Qy 961 ACCCCCAAGGCCAAGTCTGTGTGTCAGCCCACCTCAAGTCCATCTTTTGCGAGGAATTGCTG 1020
 |||
 Db 137378 ACCCCCAAGGCCAAGTCTGTGTGTCAGCCCACCTCAAGTCCATCTTTTGCGAGGAATTGCTG 137437

Qy 1021 AATAAACGCGTGGCTTGA 1038
 |||
 Db 137438 AATAAACGCGTGGCTTGA 137455

RESULT 7

EBV

LOCUS EBV 172281 bp DNA circular VRL 18-APR-2005
 DEFINITION Epstein-Barr virus (EBV) genome, strain B95-8.
 ACCESSION V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784
 VERSION V01555.1 GI:59074
 KEYWORDS DNA polymerase; EBNA; genome; ribonucleotide reductase; tandem repeat; terminal repeat.
 SOURCE Human herpesvirus 4 (Epstein-Barr virus)
 ORGANISM Human herpesvirus 4
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1
 AUTHORS Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and Griffin,B.E.
 TITLE Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments
 JOURNAL Nucleic Acids Res. 9 (13), 2999-3014 (1981)
 PUBMED 6269068

REFERENCE 2
 AUTHORS Kozak,M.
 TITLE Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes
 JOURNAL Nucleic Acids Res. 9 (20), 5233-5252 (1981)
 PUBMED 7301588

REFERENCE 3
 AUTHORS Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.
 TITLE Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome
 JOURNAL J. Cell. Biochem. 19 (3), 267-274 (1982)
 PUBMED 6296170

REFERENCE 4

AUTHORS Farrell,P.J., Bankier,A., Seguin,C., Deininger,P. and Barrell,B.G.
 TITLE Latent and lytic cycle promoters of Epstein-Barr virus
 JOURNAL EMBO J. 2 (8), 1331-1338 (1983)
 PUBMED 10872327
 REFERENCE 5
 AUTHORS Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.
 TITLE Homologous upstream sequences near Epstein-Barr virus promoters
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)
 PUBMED 6300857
 REFERENCE 6 (bases 142687 to 159853)
 AUTHORS Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.
 TITLE Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
 Epstein-Barr virus
 JOURNAL Mol. Biol. Med. 1 (1), 21-45 (1983)
 PUBMED 6092825
 REFERENCE 7 (bases 112620 to 125316)
 AUTHORS Seguin,C., Farrell,P.J. and Barrell,B.G.
 TITLE DNA sequence and transcription of the BamHI fragment B region of
 B95-8 Epstein-Barr virus
 JOURNAL Mol. Biol. Med. 1 (3), 369-392 (1983)
 PUBMED 6094953
 REFERENCE 8 (bases 45644 to 52450)
 AUTHORS Jeang,K.T. and Hayward,S.D.
 TITLE Organization of the Epstein-Barr virus DNA molecule. III. Location
 of the P3HR-1 deletion junction and characterization of the NotI
 repeat units that form part of the template for an abundant
 12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
 JOURNAL J. Virol. 48 (1), 135-148 (1983)
 PUBMED 6310141
 REFERENCE 9 (bases 159853 to 172281)
 → AUTHORS Bankier,A.T., Deininger,P.L., Satchwell,S.C., Baer,R., Farrell,P.J.
 and Barrell,B.G.
 TITLE DNA sequence analysis of the EcoRI Dhet fragment of B95-8
 Epstein-Barr virus containing the terminal repeat sequences
 JOURNAL Mol. Biol. Med. 1 (4), 425-445 (1983)
 PUBMED 6094955
 REFERENCE 10 (bases 45415 to 52824)
 AUTHORS Jones,M.D., Foster,L., Sheedy,T. and Griffin,B.E.
 TITLE The EB virus genome in Daudi Burkitt's lymphoma cells has a
 deletion similar to that observed in a non-transforming strain
 (P3HR-1) of the virus
 JOURNAL EMBO J. 3 (4), 813-821 (1984)
 PUBMED 6327290
 REFERENCE 11 (bases 87650 to 92703)
 AUTHORS Biggin,M., Farrell,P.J. and Barrell,B.G.
 TITLE Transcription and DNA sequence of the BamHI L fragment of B95-8
 Epstein-Barr virus
 JOURNAL EMBO J. 3 (5), 1083-1090 (1984)
 PUBMED 6203743
 REFERENCE 12 (bases 7315 to 9312)
 AUTHORS Yates,J., Warren,N., Reisman,D. and Sugden,B.
 TITLE A cis-acting element from the Epstein-Barr viral genome that
 permits stable replication of recombinant plasmids in latently
 infected cells
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)
 PUBMED 6328526
 REFERENCE 13 (bases 76089 to 79808)
 AUTHORS Gibson,T., Stockwell,P., Ginsburg,M. and Barrell,B.
 TITLE Homology between two EBV early genes and HSV ribonucleotide
 reductase and 38K genes
 JOURNAL Nucleic Acids Res. 12 (12), 5087-5099 (1984)

PUBMED 6330697
 REFERENCE 14 (bases 1 to 172281)
 AUTHORS Baer,R., Bankier,A.T., Biggin,M.D., Deininger,P.L., Fallell,P.J., Gibson,T.J., Hatfull,G., Hudson,G.S., Satchwell,S.C., Seguin,C., Tuffnell,P.S. and Barrell,B.G.
 TITLE DNA sequence and expression of the B95-8 Epstein-Barr virus genome
 JOURNAL Nature 310 (5974), 207-211 (1984)
 PUBMED 6087149
 REFERENCE 15
 AUTHORS Bodescot,M. and Perricaudet,M.
 TITLE Clustered alternative splice sites in Epstein-Barr virus RNAs
 JOURNAL Nucleic Acids Res. 15 (14), 5887 (1987)
 PUBMED 3039467
 REFERENCE 16
 → AUTHORS Laux,G., Perricaudet,M. and Farrell,P.J.
 TITLE A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is created by circularization of the linear viral genome
 JOURNAL EMBO J. 7 (3), 769-774 (1988)
 PUBMED 2840285
 REFERENCE 17
 AUTHORS Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
 JOURNAL Unpublished
 REFERENCE 18 (bases 1 to 172281)
 AUTHORS Farrell,P.J. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUN-1984)
 REFERENCE 19 (bases 1 to 172281)
 AUTHORS Farrell,P.J.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1988) Farrell P., Ludwig Institute for Cancer Research, St. Mary's Hospital Medical School, Norfolk Place London W2 1PG
 COMMENT On or before Apr 23, 2004 this sequence version replaced gi:330432, gi:330357, gi:330413.
 CDS
 Listed under this feature are all known protein coding regions as well as all the major open reading frames in the sequence. In general the term major is taken as the longest frame in a particular region taking into account the adjacent longest frames and likely transcription signals. Note that on this basis some long overlapping frames have been excluded and on the other hand some small frames have been included which might represent exons or genes because they occur in a logical combination with other features or because of some other experimental data. The reading frames are named according to the Bam H1 fragment in which they start. eg BALF3 is the third leftward frame starting in Bam H1 fragment A. BORF1 is the first rightward frame in Bam H1 fragment O. If there is an obvious TATA sequence followed by an in frame Met codon that satisfies the rules of Kozak [12] in that there is a purine at -3 and/or a G at +4 then the reading frame is numbered from the A of the ATG to the base preceding the termination codon. If there is no obvious initiation codon or there is a substantial reading frame in phase before the ATG then the reading frame is numbered from the first base of the first codon.
 SITES of POLYA signals
 This feature lists all occurrences of the sequence AATAAA which is found normally approximately 20 bases upstream of the mRNA processing/polyA addition site. The rarely used homolog ATTAAA is only listed when it is found in a position close to the end of a major reading frame.

SITES of DONOR and ACCEPT sequences

This is not a comprehensive listing of all such sequences and only the positions of a few have been noted because they occur in potentially interesting positions. The number quoted in the table is the position of the terminal base in the intron in each case. Restriction enzyme SITES.

Only the positions of the sites Bam HI (BAM) are listed. RPT

This feature is used to define repetitive sequences. SITE DEL

This feature defines deletions in B95-8 with respect to other strains such as RAJI and also to deletions in other strains such as P3HR1 and DAUDI with respect to B95-8.

SITE HPN

Denotes sequences with twofold symmetry ie could form hairpin loops. This is not a comprehensive list - only a few occurrences noted.

ORGRPL

Denotes the region that encompasses an origin of replication (ori P).[13].

NUMBERING

The DNA sequence of B95-8 EBV has been revised [19]. The original (Baer et al, 1984) base 359 has been deleted so the new sequence around that position reads TCAGTCTTT. To avoid renumbering the entire sequence, position 1 has been moved 1 base to the left of the EcoRI site separating EcoRI Dhet from EcoRI I (ie the first A of AGAATTC).

| FEATURES | Location/Qualifiers |
|--------------|---|
| source | 1. .172281 /organism="Human herpesvirus 4" /mol_type="genomic DNA" /strain="B95-8" /db_xref="taxon:10376" |
| mRNA | 58. .272 /product="exon 2 terminal protein RNA" |
| mRNA | 360. .458 /product="exon 3 terminal protein RNA" |
| misc_feature | complement(535) /note="polyA signal: AATAAA" |
| mRNA | 540. .788 /product="exon 4 terminal protein RNA" |
| mRNA | 871. .951 /product="exon 5 terminal protein RNA" |
| mRNA | 1026. .1196 /product="exon 6 terminal protein RNA" |
| promoter | complement(1192) /note="TATA: TATAAAT" |
| mRNA | 1280. .1495 /product="exon 7 terminal protein RNA" |
| promoter | complement(1383) |

Query Match 100.0%; Score 1038; DB 13; Length 172281;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ATGCTATCAGGTAACGCAGGAGAAGGAGCAACAGCCTGCGGAGGTTCGGCCGCCGCGGGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      148707 ATGCTATCAGGTAACGCAGGAGAAGGAGCAACAGCCTGCGGAGGTTCGGCCGCCGCGGGC 148766

Qy      61 CAGGACCTCATCAGCGTCCCCCGCAACACCTTTATGACACTGCTTCAGACCAACCTGGAC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      148767 CAGGACCTCATCAGCGTCCCCCGCAACACCTTTATGACACTGCTTCAGACCAACCTGGAC 148826

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| | | | |
|----|--------|--|--------|
| Qy | 121 | AACAAACCGCCGAGGCAGACCCCGCTACCCTACGCGGCCCGCTGCCCCCTTTTCCCAC | 180 |
| | | | |
| Db | 148827 | AACAAACCGCCGAGGCAGACCCCGCTACCCTACGCGGCCCGCTGCCCCCTTTTCCCAC | 148886 |
| Qy | 181 | CAGGCAATAGCCACCGCGCCTTCCTACGGTCCTGGGGCCGGAGCGGTCGCCCCGGCCGGC | 240 |
| | | | |
| Db | 148887 | CAGGCAATAGCCACCGCGCCTTCCTACGGTCCTGGGGCCGGAGCGGTCGCCCCGGCCGGC | 148946 |
| Qy | 241 | GGCTACTTTACCTCCCCAGGAGGTTACTACGCCGGGCCCGCGGGCGGGGACCCGGGTGCC | 300 |
| | | | |
| Db | 148947 | GGCTACTTTACCTCCCCAGGAGGTTACTACGCCGGGCCCGCGGGCGGGGACCCGGGTGCC | 149006 |
| Qy | 301 | TTCTTGGCGATGGACGCTCACACCTACCACCCCCACCCACACCCCCCTCCGGCCTACTTT | 360 |
| | | | |
| Db | 149007 | TTCTTGGCGATGGACGCTCACACCTACCACCCCCACCCACACCCCCCTCCGGCCTACTTT | 149066 |
| Qy | 361 | GGCTTGCCGGGCCTCTTTGGCCCCCTCCACCCGTGCCTCCTTACTACGGATCCCCTTG | 420 |
| | | | |
| Db | 149067 | GGCTTGCCGGGCCTCTTTGGCCCCCTCCACCCGTGCCTCCTTACTACGGATCCCCTTG | 149126 |
| Qy | 421 | CGGGCAGACTACGTCCCCGCTCCCTCGCGATCCAACAAGCGGAAAAGAGACCCCGAGGAG | 480 |
| | | | |
| Db | 149127 | CGGGCAGACTACGTCCCCGCTCCCTCGCGATCCAACAAGCGGAAAAGAGACCCCGAGGAG | 149186 |
| Qy | 481 | GATGAAGAAGGCGGGGGCTATTCCCGGGGAGGACGCCACCCTCTACCGCAAGGACATA | 540 |
| | | | |
| Db | 149187 | GATGAAGAAGGCGGGGGCTATTCCCGGGGAGGACGCCACCCTCTACCGCAAGGACATA | 149246 |
| Qy | 541 | GCGGGCCTCTCCAAGAGTGTGAATGAGTTACAGCACACGCTACAGGCCCTGCGCCGGGAG | 600 |
| | | | |
| Db | 149247 | GCGGGCCTCTCCAAGAGTGTGAATGAGTTACAGCACACGCTACAGGCCCTGCGCCGGGAG | 149306 |
| Qy | 601 | ACGCTGTCCTACGGCCACACCGGAGTCGGATACTGCCCCAGCAGGGCCCCTGCTACACC | 660 |
| | | | |
| Db | 149307 | ACGCTGTCCTACGGCCACACCGGAGTCGGATACTGCCCCAGCAGGGCCCCTGCTACACC | 149366 |
| Qy | 661 | CACTCGGGGCCTTACGGATTTTCAGCCTCATCAAAGCTACGAAGTGCCAGATACGTCCCT | 720 |
| | | | |
| Db | 149367 | CACTCGGGGCCTTACGGATTTTCAGCCTCATCAAAGCTACGAAGTGCCAGATACGTCCCT | 149426 |
| Qy | 721 | CATCCGCCCCCACCACCAACTTCTCACCAGGCAGCTCAGGCGCAGCCTCCACCCCCGGGC | 780 |
| | | | |
| Db | 149427 | CATCCGCCCCCACCACCAACTTCTCACCAGGCAGCTCAGGCGCAGCCTCCACCCCCGGGC | 149486 |
| Qy | 781 | ACACAGGCCCCGAAGCCCACTGTGTGGCCGAGTCCACGATCCCTGAGGCGGGAGCAGCC | 840 |
| | | | |
| Db | 149487 | ACACAGGCCCCGAAGCCCACTGTGTGGCCGAGTCCACGATCCCTGAGGCGGGAGCAGCC | 149546 |
| Qy | 841 | GGGAACTCTGGACCCCGGGAGGACACCAACCCTCAGCAGCCCACCACCGAGGGCCACCAC | 900 |
| | | | |
| Db | 149547 | GGGAACTCTGGACCCCGGGAGGACACCAACCCTCAGCAGCCCACCACCGAGGGCCACCAC | 149606 |
| Qy | 901 | CGCGGAAAGAACTGGTGCAGGCCTCTGCGTCCGGAGTGGCTCAGTCTAAGGAGCCCACC | 960 |
| | | | |
| Db | 149607 | CGCGGAAAGAACTGGTGCAGGCCTCTGCGTCCGGAGTGGCTCAGTCTAAGGAGCCCACC | 149666 |
| Qy | 961 | ACCCCCAAGGCCAAGTCTGTGTCAGCCACCTCAAGTCCATCTTTTGCGAGGAATTGCTG | 1020 |
| | | | |
| Db | 149667 | ACCCCCAAGGCCAAGTCTGTGTCAGCCACCTCAAGTCCATCTTTTGCGAGGAATTGCTG | 149726 |
| Qy | 1021 | AATAAACGCGTGGCTTGA | 1038 |

Db 149727 AATAACGCGTGGCTTGA 149744

RESULT 8

HS4B958RAJ

LOCUS HS4B958RAJ 184113 bp DNA linear VRL 12-APR-1996

DEFINITION Epstein-Barr virus, artifactual joining of B95-8 complete genome and the sequences from Raji of the large deletion found in B95-8.

ACCESSION M80517 M75989

VERSION M80517.1 GI:330330

KEYWORDS

SOURCE Human herpesvirus 4. (Epstein-Barr virus)

ORGANISM Human herpesvirus 4

Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1 (sites)

AUTHORS Baer,R.J., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J., Gibson,T.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C., Tuffnell,P.S. and Barrell,B.G.

TITLE DNA sequence and expression of the B95-8 Epstein-Barr virus genome

JOURNAL Nature 310 (5974), 207-211 (1984)

PUBMED 6087149

REFERENCE 2 (sites)

AUTHORS Parker,B.D., Bankier,A., Satchwell,S., Barrell,B. and Farrell,P.J.

TITLE Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region

JOURNAL Virology 179 (1), 339-346 (1990)

PUBMED 2171209

REFERENCE 3 (sites)

AUTHORS Sample,J., Brooks,L., Sample,C., Young,L., Rowe,M., Gregory,C., Rickinson,A. and Kieff,E.

TITLE Restricted Epstein-Barr virus protein expression in Burkitt lymphoma is due to a different Epstein-Barr nuclear antigen 1 transcriptional initiation site

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6343-6347 (1991)

PUBMED 1648738

REFERENCE 4 (bases 1 to 184113)

AUTHORS Jenson,H.B.

TITLE GenBank Curator Program

JOURNAL Unpublished (1992)

COMMENT Original source text: Human herpesvirus 4 DNA.

The B95-8 genome (V01555) has a large deletion in the right side of the genome which has been sequenced in Raji (M35547). These sequences have been joined to form an extended and more complete, although artifactual, EBV sequence.

For features, refer to feature tables of V01555 and M35547.

FEATURES Location/Qualifiers

source 1. .184113
/organism="Human herpesvirus 4"
/mol_type="genomic DNA"
/db_xref="taxon:10376"

misc_feature 1. .152008
/note="B95-8 sequences (corresponds to 1-152,008 of V01555)"

misc_feature 152009. .152012
/note="Overlap of B95-8 and Raji sequences at B95-8 deletion point (corresponds to 152,009-152,012 in V01555, and 1-4 in M35547)"

misc_feature 153013. .163839
/note="Raji sequences (corresponds to 5-11,831 of M35547)"

420 \$ 5

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=84270667; PubMed=6087149; DOI=10.1038/310207a0;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tuffnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=86045997; PubMed=2998075;
 RA Hudson G.S., Gibson T.J., Barrell B.G.;
 RT "The BamHI F region of the B95-8 Epstein-Barr virus genome.";
 RL Virology 147:99-109(1985).
 CC -----
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 CC -----
 DR EMBL; V01555; CAA24838.1; ALT_INIT; Genomic_DNA.
 DR EMBL; M11923; AAA45870.1; -; Genomic_DNA.
 DR InterPro; IPR009299; Herpes_capsid.
 DR Pfam; PF06112; Herpes_capsid; 1.
 KW Capsid protein; Virion protein.
 FT CHAIN 1 176 Capsid protein VP26.
 FT /FTid=PRO_0000115739.
 SQ SEQUENCE 176 AA; 18147 MW; DAB605ED00F1A656 CRC64;
 Query Match 100.0%; Score 130; DB 1; Length 176;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDTGSGGGGQPHDTAPRGARKKQ 24
 |||||
 Db 153 AVDTGSGGGGQPHDTAPRGARKKQ 176

RESULT 2

Q777G5_EBVG
 ID Q777G5_EBVG PRELIMINARY; PRT; 176 AA.
 AC Q777G5;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 13-JUN-2006, entry version 11.
 DE Capsid protein VP26.
 GN Name=BFRF3;
 OS Epstein-Barr virus (strain GD1) (HHV-4) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10376;
 OH NCBI_TaxID=9606; Homo sapiens (Human).
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=84270667; PubMed=6087149; DOI=10.1038/310207a0;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tuffnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B95-8;
 RX MEDLINE=88283646; PubMed=2840285;
 → RA Laux G., Perricaudet M., Farrell P.J.;
 RT "A spliced Epstein-Barr virus gene expressed in immortalized
 RT lymphocytes is created by circularization of the linear viral
 RT genome.";
 RL EMBO J. 7:769-774(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=82014887; PubMed=6269068;
 RA Arrand J.R., Rymo L., Walsh J.E., Bjorck E., Lindahl T., Griffin B.E.;
 RT "Molecular cloning of the complete Epstein-Barr virus genome as a set
 RT of overlapping restriction endonuclease fragments.";
 RL Nucleic Acids Res. 9:2999-3014(1981).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=82059504; PubMed=7301588;
 RA Kozak M.;
 RT "Possible role of flanking nucleotides in recognition of the AUG
 RT initiator codon by eukaryotic ribosomes.";
 RL Nucleic Acids Res. 9:5233-5252(1981).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=83109311; PubMed=6296170;
 RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
 RT "Sequence analysis and in vitro transcription of portions of the
 RT Epstein-Barr virus genome.";
 RL J. Cell. Biochem. 19:267-274(1982).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=83169725; PubMed=6300857;
 RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
 RT "Homologous upstream sequences near Epstein-Barr virus promoters.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=85035713; PubMed=6092825;
 → RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
 RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
 RT Epstein-Barr virus.";
 RL Mol. Biol. Med. 1:21-45(1983).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=85060424; PubMed=6094953;
 RA Seguin C., Farrell P.J., Barrell B.G.;
 RT "DNA sequence and transcription of the BamHI fragment B region of B95-
 RT 8 Epstein-Barr virus.";
 RL Mol. Biol. Med. 1:369-392(1983).
 RN [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=83294686; PubMed=6310141;
 RA Jeang K.T., Hayward S.D.;
 RT "Organization of the Epstein-Barr virus DNA molecule. III. Location of
 RT the P3HR-1 deletion junction and characterization of the NotI repeat

RT units that form part of the template for an abundant 12-O-
RT tetradecanoylphorbol-13-acetate-induced mRNA transcript.";
RL J. Virol. 48:135-148(1983).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=85060428; PubMed=6094955;
RA Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.,
RA Barrell B.G.;
RT "DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-
RT Barr virus containing the terminal repeat sequences.";
RL Mol. Biol. Med. 1:425-445(1983).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=20331131; PubMed=10872327;
RA Farrell P.J., Bankier A., Seguin C., Deininger P., Barrell B.G.;
RT "Latent and lytic cycle promoters of Epstein-Barr virus.";
RL EMBO J. 2:1331-1338(1983).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=84207939; PubMed=6327290;
RA Jones M.D., Foster L., Sheedy T., Griffin B.E.;
RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion
RT similar to that observed in a non-transforming strain (P3HR-1) of the
RT virus.";
RL EMBO J. 3:813-821(1984).
RN [13]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=84236104; PubMed=6203743;
RA Biggin M., Farrell P.J., Barrell B.G.;
RT "Transcription and DNA sequence of the BamHI L fragment of B95-8
RT Epstein-Barr virus.";
RL EMBO J. 3:1083-1090(1984).
RN [14]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=84222045; PubMed=6328526;
RA Yates J., Warren N., Reisman D., Sugden B.;
RT "A cis-acting element from the Epstein-Barr viral genome that permits
RT stable replication of recombinant plasmids in latently infected
RT cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
RN [15]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=84247360; PubMed=6330697;
RA Gibson T.J., Stockwell P., Ginsburg M., Barrell B.G.;
RT "Homology between two EBV early genes and HSV ribonucleotide reductase
RT and 38K genes.";
RL Nucleic Acids Res. 12:5087-5099(1984).
RN [16]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B95-8;
RX MEDLINE=87289053; PubMed=3039467;
RA Bodescot M., Perricaudet M.;
RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";
RL Nucleic Acids Res. 15:5887-5887(1987).
RN [17]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=91021036; PubMed=2171209;
 RA Parker B.D., Bankier A., Satchwell S., Barrell B., Farrell P.J.;
 RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning
 RT the B95-8 deletion region.";
 RL Virology 179:339-346(1990).
 RN [18]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RA Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [19]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RA Binne U.K., Amon W., Farrell P.J.;
 RT "Induction of Epstein-Barr virus late promoters on small plasmids in
 RT the EBV late lytic cycle requires ori lyt.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 CC -----
 DR EMBL; AJ507799; CAD53401.1; -; Genomic_DNA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR InterPro; IPR009299; Herpes_capsid.
 DR Pfam; PF06112; Herpes_capsid; 1.
 SQ SEQUENCE 176 AA; 18147 MW; DAB605ED00F1A656 CRC64;

Query Match 100.0%; Score 130; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDTGSGGGGQPHDTAPRGARKKQ 24
 |||||
 Db 153 AVDTGSGGGGQPHDTAPRGARKKQ 176

RESULT 3

Q3KSU9_EBVG

ID Q3KSU9_EBVG PRELIMINARY; PRT; 176 AA.
 AC Q3KSU9;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 11-JUL-2006, entry version 10.
 DE Hypothetical protein (BFRF3).
 OS Epstein-Barr virus (strain GD1) (HHV-4) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10376;
 OH NCBI_TaxID=9606; Homo sapiens (Human).
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GD1;
 RX PubMed=16306603; DOI=10.1128/JVI.79.24.15323-15330.2005;
 RA Zeng M.-S., Li D.-J., Liu Q.-L., Song L.-B., Li M.-Z., Zhang R.-H.,
 RA Yu X.-J., Wang H.-M., Ernberg I., Zeng Y.-X.;
 RT "Genomic sequence analysis of Epstein-Barr virus strain GD1 from a
 RT nasopharyngeal carcinoma patient.";
 RL J. Virol. 79:15323-15330(2005).
 RN [2]

SEQ 1 of 10/036,729

QY 481 TGGCGGGGGACAACCCACGACACCGCCCCACGCGGGGCACGTAAGAAACAGTAG 535
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7130 TGGCGGGGGACAACCCACGACACCGCCCCACGCGGGGCACGTAAGAAACAGTAG 7184

RESULT 7
 HHV507799

LOCUS HHV507799 171823 bp DNA circular VRL 15-APR-2005

DEFINITION Human herpesvirus 4 complete wild type genome.

ACCESSION AJ507799

VERSION AJ507799.1 GI:23893576

KEYWORDS complete genome.

SOURCE Human herpesvirus 4 (Epstein-Barr virus)

ORGANISM Human herpesvirus 4

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE

1
 AUTHORS Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and
 Griffin,B.E.

TITLE Molecular cloning of the complete Epstein-Barr virus genome as a
 set of overlapping restriction endonuclease fragments

JOURNAL Nucleic Acids Res. 9 (13), 2999-3014 (1981)

PUBMED 6269068

REFERENCE

2
 AUTHORS Kozak,M.

TITLE Possible role of flanking nucleotides in recognition of the AUG
 initiator codon by eukaryotic ribosomes

JOURNAL Nucleic Acids Res. 9 (20), 5233-5252 (1981)

PUBMED 7301588

REFERENCE

3
 AUTHORS Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.
 TITLE Sequence analysis and in vitro transcription of portions of the
 Epstein-Barr virus genome

JOURNAL J. Cell. Biochem. 19 (3), 267-274 (1982)

PUBMED 6296170

REFERENCE

4
 AUTHORS Farrell,P.J., Bankier,A., Seguin,C., Deininger,P. and Barrell,B.G.
 TITLE Latent and lytic cycle promoters of Epstein-Barr virus

JOURNAL EMBO J. 2 (8), 1331-1338 (1983)

PUBMED 10872327

REFERENCE

5
 AUTHORS Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.

TITLE Homologous upstream sequences near Epstein-Barr virus promoters

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)

PUBMED 6300857

REFERENCE

6
 AUTHORS Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.

TITLE Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
 Epstein-Barr virus

JOURNAL Mol. Biol. Med. 1 (1), 21-45 (1983)

PUBMED 6092825

REFERENCE

7
 AUTHORS Seguin,C., Farrell,P.J. and Barrell,B.G.

TITLE DNA sequence and transcription of the BamHI fragment B region of
 B95-8 Epstein-Barr virus

JOURNAL Mol. Biol. Med. 1 (3), 369-392 (1983)

PUBMED 6094953

REFERENCE

8
 AUTHORS Jeang,K.T. and Hayward,S.D.

TITLE Organization of the Epstein-Barr virus DNA molecule. III. Location

of the P3HR-1 deletion junction and characterization of the NotI repeat units that form part of the template for an abundant 12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript

JOURNAL
PUBMED

6310141

REFERENCE

9

AUTHORS

Bankier, A.T., Deininger, P.L., Satchwell, S.C., Baer, R., Farrell, P.J. and Barrell, B.G.

TITLE

DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-Barr virus containing the terminal repeat sequences

JOURNAL

Mol. Biol. Med. 1 (4), 425-445 (1983)

PUBMED

6094955

REFERENCE

10

AUTHORS

Jones, M.D., Foster, L., Sheedy, T. and Griffin, B.E.

TITLE

The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion similar to that observed in a non-transforming strain (P3HR-1) of the virus

JOURNAL

EMBO J. 3 (4), 813-821 (1984)

PUBMED

6327290

REFERENCE

11

AUTHORS

Biggin, M., Farrell, P.J. and Barrell, B.G.

TITLE

Transcription and DNA sequence of the BamHI L fragment of B95-8 Epstein-Barr virus

JOURNAL

EMBO J. 3 (5), 1083-1090 (1984)

PUBMED

6203743

REFERENCE

12

AUTHORS

Yates, J., Warren, N., Reisman, D. and Sugden, B.

TITLE

A cis-acting element from the Epstein-Barr viral genome that permits stable replication of recombinant plasmids in latently infected cells

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)

PUBMED

6328526

REFERENCE

13

AUTHORS

Gibson, T., Stockwell, P., Ginsburg, M. and Barrell, B.

TITLE

Homology between two EBV early genes and HSV ribonucleotide reductase and 38K genes

JOURNAL

Nucleic Acids Res. 12 (12), 5087-5099 (1984)

PUBMED

6330697

REFERENCE

14 (bases 1 to 171823)

AUTHORS

Baer, R.J., Bankier, A.T., Biggin, M.D., Deininger, P.L., Farrell, P.J., Gibson, T.J., Hatfull, G.F., Hudson, G.S., Satchwell, S.C., Seguin, C., Tuffnell, P.S. and Barrell, B.G.

TITLE

DNA sequence and expression of the B95-8 Epstein-Barr virus genome

JOURNAL

Nature 310 (5974), 207-211 (1984)

PUBMED

6087149

REFERENCE

15

AUTHORS

Bodescot, M. and Perricaudet, M.

TITLE

Clustered alternative splice sites in Epstein-Barr virus RNAs

JOURNAL

Nucleic Acids Res. 15 (14), 5887 (1987)

PUBMED

3039467

REFERENCE

16

AUTHORS

Laux, G., Perricaudet, M. and Farrell, P.J.

TITLE

A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is created by circularization of the linear viral genome

JOURNAL

EMBO J. 7 (3), 769-774 (1988)

PUBMED

2840285

REFERENCE

17

AUTHORS

Parker, B.D., Bankier, A., Satchwell, S., Barrell, B. and Farrell, P.J.

TITLE

Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region

JOURNAL Virology 179 (1), 339-346 (1990)
PUBMED 2171209
REFERENCE 18 (bases 1 to 171823)
AUTHORS Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
JOURNAL Unpublished
REFERENCE 19
AUTHORS Binne,U.K., Amon,W. and Farrell,P.J.
TITLE Induction of Epstein-Barr virus late promoters on small plasmids in the EBV late lytic cycle requires ori lyt
JOURNAL Unpublished
REFERENCE 20 (bases 1 to 171823)
AUTHORS Farrell,P.J.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2002) Farrell P., Ludwig Institute for Cancer Research, Imperial College School of Medicine, St. Mary's Campus, Norfolk Place London W2 1PG
COMMENT Construction:
This sequence was assembled from B95-8 EBV [14] and Raji EBV [18] with sequence corrections [16, 19]. The number of major internal repeat units has been reduced from 11.6 [14] to a more typical 7.6 and the B95-8 deletion sequences have been restored to give a sequence more representative of wild type EBV.
Numbering
Like the modified B95-8 sequence[14, 16] accession number V01555, this sequence starts 1 base to the left of the EcoRI site separating EcoRI Dhet from EcoRI I (ie the first A of AGAATTC.).
FEATURES
source Location/Qualifiers
1. .171823
/organism="Human herpesvirus 4"
/mol_type="genomic DNA"
/strain="B95-8"
/db_xref="taxon:10376"
source 139724. .151554
/organism="Human herpesvirus 4"
/mol_type="genomic DNA"
/strain="Raji"
/db_xref="taxon:10376"
CDS join(166103. .166458,58. .272,360. .458,540. .788,871. .951,1026. .1196,1280. .1495,1574. .1680)
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Query Match 98.8%; Score 531.8; DB 13; Length 171823;
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Matches 533; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Qy | 61 | AGACAGTCCCCTGCTTCCTAAATTTCAAGAGCTGAACCAGAATAATCTCCCCAATGATGT | 120 |
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| Db | 49335 | TTTTCGGGAGGCTCAAAGAAGTTACCTGGTATTTCTGACATCCCAGTTCTGCTACGAAGA | 49394 |
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| Qy | 361 | CACGGCCGTAGCCCAGTCCGCGACCCCCTCTGTTTCTTCATCTATTAGCAGCCTCCGGGC | 420 |
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| Db | 49635 | CGCGACTTCGGGGGCGACTGCCGCCGCCTCCGCCGCCGACCCGTCGATACCGGGTCAGG | 49694 |

Qy 481 TGGCGGGGGACAACCCACGACACCGCCCCACGCGGGGCACGTAAGAAACAGTAG 535
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RESULT 8

EBV

LOCUS EBV 172281 bp DNA circular VRL 18-APR-2005

DEFINITION Epstein-Barr virus (EBV) genome, strain B95-8.

ACCESSION V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784

VERSION V01555.1 GI:59074

KEYWORDS DNA polymerase; EBNA; genome; ribonucleotide reductase; tandem repeat; terminal repeat.

SOURCE Human herpesvirus 4 (Epstein-Barr virus)

ORGANISM Human herpesvirus 4

Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE

1

AUTHORS Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and Griffin,B.E.

TITLE Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments

JOURNAL Nucleic Acids Res. 9 (13), 2999-3014 (1981)

PUBMED 6269068

REFERENCE

2

AUTHORS Kozak,M.

TITLE Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes

JOURNAL Nucleic Acids Res. 9 (20), 5233-5252 (1981)

PUBMED 7301588

REFERENCE

3

AUTHORS Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.

TITLE Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome

JOURNAL J. Cell. Biochem. 19 (3), 267-274 (1982)

PUBMED 6296170

REFERENCE

4

AUTHORS Farrell,P.J., Bankier,A., Seguin,C., Deininger,P. and Barrell,B.G.

TITLE Latent and lytic cycle promoters of Epstein-Barr virus

JOURNAL EMBO J. 2 (8), 1331-1338 (1983)

PUBMED 10872327

REFERENCE

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AUTHORS Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.

TITLE Homologous upstream sequences near Epstein-Barr virus promoters

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)

PUBMED 6300857

REFERENCE

6 (bases 142687 to 159853)

AUTHORS Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.

TITLE Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8 Epstein-Barr virus

JOURNAL Mol. Biol. Med. 1 (1), 21-45 (1983)

PUBMED 6092825

REFERENCE

7 (bases 112620 to 125316)

AUTHORS Seguin,C., Farrell,P.J. and Barrell,B.G.

TITLE DNA sequence and transcription of the BamHI fragment B region of B95-8 Epstein-Barr virus

JOURNAL Mol. Biol. Med. 1 (3), 369-392 (1983)

PUBMED 6094953

REFERENCE

8 (bases 45644 to 52450)

AUTHORS Jeang,K.T. and Hayward,S.D.